

34 312.6 33.0 618 10 AF003523 Rattus no
c 267.2 28.2 445 6 AX407708 Sequence
c 245.6 26.0 338 11 G38672 SHG-54070
37 226.8 24.0 779 10 AF279911 Rattus no
38 197.2 20.8 270 6 AX886392 Sequence
39 197.2 20.8 270 6 BD026002 Sequence
40 197 20.8 230039 2 AC090391 Homo sapi
c 41 195.6 20.7 2187 6 AX882875 Sequence
c 42 195.6 20.7 2187 6 BD159979 Primer fo
c 43 195.6 20.7 2187 9 AK023420 Homo sapi
c 44 192.6 20.4 225 9 HS164B9F 257098 H.sapiens C
45 189 20.0 189 6 AR027724 Sequence AR027724

ALIGNMENTS

RESULT 1
AR079500
LOCUS AR079500 946 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 1 from patent US 5965703.
ACCESSION AR079500
VERSION AR079500.1 GI:10006244
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
Unclassified.
1 (bases 1 to 946)
AUTHORS Horne,W.A. and Oltersdorf,T.
TITLE Human bad polypeptides, encoding nucleic acids and methods of use
JOURNAL Patent: US 5965703-A 1 12-OCT-1999;
FEATURES
Location/Qualifiers
source 1..946
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 946; DB 6; Length 946;
Best Local Similarity 100.0%; Pred. No. 4.5e-186;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGGCTAGGGCCCGGGCTCAGGGGCTCGAGATCGGGCTTGGGCCGAGCATGTTCCAG 60
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Db 61 ATCCAGAGTTTGAGCCGAGTGAGCAGGAAGACTCCAGCTCTGACAGAGGGGCGCTGGGC 120
Qy 121 CCCAGCCCCGACGAGGGAACGGGCGCTTCAGGCTCCGGGAAGCATCATCCGAGGCCCGACGC 180
Db 121 CCCAGCCCCGACGAGGGAACGGGCGCTTCAGGCTCCGGGAAGCATCATCCGAGGCCCGACGC 180
Qy 181 CTCCTGTGGGACGCCAGTCAACACGAGGAGCAGCAACACGAGGAGCCATCATGGAGGC 240
Db 181 CTCCTGTGGGACGCCAGTCAACACGAGGAGCAGCAACACGAGGAGCCATCATGGAGGC 240

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Db 361 CTCTGGGCACGACAGCGCTATGCCCGCAGCTCCGGAGGATGAGTGACGAGTTTGTGGAC 420
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Db 541 TCCGCCCCCTCCCGAGTGAACCTTCGGTCCACATCCCGAAATCCACCCGTTCCCATTTGCCCT 600
Qy 601 GGGAGCCATTTGAATATGGGAGGAAGTAAGTTCCCTCAGGCTATGCAAAAGAGAT 660
Db 601 GGGAGCCATTTGAATATGGGAGGAAGTAAGTTCCCTCAGGCTATGCAAAAGAGAT 660
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RESULT 2

AR274069
LOCUS AR274069 946 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1 from patent US 6504022.
ACCESSION AR274069
VERSION AR274069.1 GI:29705040
KEYWORDS
SOURCE Unknown.

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Qy	901	GTACCAAAATGTTAATAAGCCGCCGTGTGTGCCAAAAA	946
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LOCUS	BD062656	946 bp	DNA linear PAT 27-AUG-2002
DEFINITION	Human BAD polypeptides, encoding nucleic acids and methods of use.		
ACCESSION	BD062656		
VERSION	BD062656.1	GI:22608259	
KEYWORDS	JP 2001507211-A/1.		
SOURCE	Rattus norvegicus		
ORGANISM	Rattus norvegicus		
REFERENCE	1 (bases 1 to 946)		
AUTHORS	Horne, W.A. and Oltersdorf, T.		
TITLE	Human BAD polypeptides, encoding nucleic acids and methods of use		
JOURNAL	Patent: JP 2001507211-A 1 05-JUN-2001;		
COMMENT	IDUN PHARMACEUTICALS INC		
	PN JP 2001507211-A/1		
	PD 05-JUN-2001		
	PF 18-SEP-1997 JP 1998514997		
	PR 20-SEP-1996 US 08/717123		
	PI WILLIAM A HORNE, TILMAN OLTERSDORF		
	PC C12N15/09, A61K45/00, A61P43/00, C07K14/47, C12Q1/02, G01N33/15, PC		
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	CC Strandedness: Single;		
	CC Topology: Linear;		
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Matches 946;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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Qy	61	ATCCAGATTTGAGCCGATGACGAGGAAGATCTCAGCTGTGCAGAGAGGGGCTGGGC	120

Db	61	ATCCAGAGTTTGGAGCCGAGTGAGCAGGAAGACTCCAGCTCTGCAGAGAGGGCTGGGC	120
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Db	121	CCAGCCCGCGAGGGACGGGCGCTCAGGCTCGGAAGCATCATCGCCAGGCCCGCAGGC	180
Qy	181	CTCCTGTGGGCGCGCAGTCACAGCAGGAGCCAAACAGCAGCAGCAGCATCATGGAGGC	240
Db	181	CTCCTGTGGGCGCGCAGTCACAGCAGGAGCCAAACAGCAGCAGCAGCATCATGGAGGC	240
Qy	241	GCTGGGCTGTGGAGATCGGAGTCGCCAGAGCTCTACCCCGCGGGACGGAGGACGAC	300
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Qy	301	GAAGGATGGGAGAGGCCAGCCCTTTTCGGGGCGCTCGCGCTCGGGCGCCGCCAAC	360
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Qy	841	AGGTTTAAACGTTGTGTACCGGAGCCGAGCCCGCGATGCCCTGGGGGCGGTATCA	900
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Qy	901	GTACCAATGTTAATAAGCCCGCTGTGTGCCAAAAA 946	

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Run on: May 28, 2004, 13:19:03 ; Search time 460 Seconds
(without alignments)
8736.512 Million cell updates/sec

Title: US-09-922-378-1
Perfect score: 946
Sequence: 1 gggctaggcgccgggtca.....gtgtgcaaaaaaaaaa 946

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues 6747726
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
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1	945	99.9	945 7	AB281200	Human BAD
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5	799	84.5	953 6	ABL61922	Colo ad
6	737	77.9	944 2	AAH91561	BGCs Gene
7	546	57.7	842 6	ABQ54707	Human Ova

8	507	53.6	507	4	AA84599	Human Bad
9	400	42.3	477	8	ACH40355	Human foe
10	381.2	40.3	449	8	ACH39197	Human mit
11	346	36.6	442	9	ADD32823	Human mit
12	344	36.4	1454	7	AB281201	Murine BA
13	344	36.4	1472	2	AAT29479	bcl-x(L)/
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15	331	35.0	1015	9	ADB53076	Primary r
16	327.2	34.6	615	2	AAV27833	Murine BC
17	325.6	34.4	615	2	AAV27835	Mutant BC
18	324	34.2	615	2	AAV27834	Mutant BC
19	324	34.2	615	2	AAV27836	Mutant BC
20	322.4	34.1	1704	5	AA800248	Bad-DTR
21	267.2	28.2	445	6	ABN93857	Gene #355
22	246.4	26.0	338	9	ADD32822	Human mit
23	197.2	20.8	270	3	AAC02257	Human sec
24	195.6	20.7	2187	4	AAH17987	Human cdn
25	190	20.1	190	2	AAV27838	Mutant BC
26	190	20.1	190	2	AAV27837	Mutant BC
27	188.4	19.9	190	2	AAV27839	Mutant BC
28	186.8	19.7	190	2	AAV27840	Mutant BC
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30	122.2	12.9	654	6	ABQ16860	Oligonuel
31	122.2	12.9	654	6	ABQ16861	Oligonuel
32	110.8	11.7	654	6	ABQ16858	Oligonuel
33	110.8	11.7	654	6	ABQ16859	Oligonuel
34	106.2	11.2	17580	6	ABL54312	Chemical
35	106.2	11.2	17580	6	ABN80013	Human che
36	98.6	10.4	17580	6	ABL54311	Chemical
37	98.6	10.4	17580	6	ABN80012	Human che
38	77.4	8.2	548	8	ACC83424	BAD hypox
39	64.4	6.8	890	8	ACC83412	Hypoxia e
40	64	6.8	525	4	AAH07259	Human cdn
41	60	6.3	60	6	ABN40532	Human spl
42	55.8	5.9	2000	7	ADA71938	Rice gene
43	49.6	5.2	2000	7	ADA71938	Rice gene
44	49.4	5.2	51	4	AAI33481	Human SNP
45	49.4	5.2	51	4	AAH79586	Human DNA

ALIGNMENTS

RESULT 1
AB281200
ID AB281200 standard; cDNA; 945 BP.
XX
AC AB281200;
XX
DT 10-MAY-2003 (first entry)
XX
DE Human BAD encoding cDNA SEQ ID NO:1.
XX
KW Human; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
XX
KW virucide; infection; gene; ss.
XX
OS Homo sapiens.

Best Local Similarity 99.8%; Pred. No. 4.8e-225; Matches 944; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGCTTAGGGCGCGGGCTCAGGGGCTCAGAGATCGGGCTTGGGCGCAGAGCATGTTCAG 60
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Qy 781 CGGTGCGGCGGCTCAGGTTCCGCGGTTTCCCGAGGCGCTCGCTAAGTAGAGAGAG 840

ID AAV25877 standard; cDNA; 946 BP.
XX AC AAV25877;
XX DT 17-JUL-1998 (first entry)
XX DE cDNA for human Bcl-xL/Bcl-2 associated death promoting polypeptide.
XX KW Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;
XX OS programmed cell death; apoptosis; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 52..558
XX FT /*tag= a
XX FT /product= "Bad"
XX PN M09812328-A2.
XX PD 26-MAR-1998.
XX PF 18-SEP-1997; 97WO-US016991.
XX PR 20-SEP-1996; 96US-00717123.
XX PA (IDUN-) IDUN PHARM INC.
XX PI Horne WA, Oltersdorf T;
XX DE WPI; 1998-217267/19.
XX DR P-PSDB; AAN55779.
XX FT Bad gene mediating apoptosis - used to develop products for treating e.g.
XX PS neurodegenerative disease, cancers or autoimmune disease.
XX PS Claim 2; Fig 1; 4lpp; English.
XX CC The present sequence encodes the human Bcl-xL/Bcl-2 associated death
XX CC promoting polypeptide, Bad, the binding of which to Bcl-XL results in the
XX CC induction of programmed cell death, i.e. apoptosis. Bad can be used in
XX CC screening assays for compounds to treat or prevent diseases characterised
XX CC by apoptotic cell death, such as neurodegenerative disorders, e.g.
XX CC Alzheimer's and Parkinson's disease, amyotrophic lateral sclerosis,
XX CC retinitis pigmentosa and cerebellar degeneration, and myelodysplastic
XX CC syndromes, e.g. aplastic anaemia and ischaemic injury including
XX CC myocardial infarction, stroke and reperfusion injury. Assays can also be
XX CC used to obtain apoptosis enhancing compounds to treat or prevent diseases
XX CC characterised by the loss of apoptotic cell death, such as cancers, e.g.
XX CC lymphoma and hormone dependent tumours, autoimmune diseases, e.g.
XX CC systemic lupus erythematosus and immune-mediated glomerulonephritis and
XX CC viral infections, e.g. herpesvirus, poxvirus or adenovirus infection. Bad
XX CC can also be used for detection and diagnosis
SQ Sequence 946 BP; 186 A; 295 C; 309 G; 156 T; 0 U; 0 Other;

Query Watch 99.7%; Score 942.8; DB 2; Length 946;

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Db 841 AGGTTTAACCGTTGTCTACCGGGACCCGAGCCCGCCGATGCCCTGGGGGCGGTGATCA 900
Qy 901 GTACCAATGTTAATAAGCCCGCGTGTGTGCCAATAAAAAAAAAAAAAA 946
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Job time : 467 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on: May 28, 2004, 22:04:17 ; Search time 499 Seconds
(without alignments)
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Title: US-09-922-378-1
Perfect score: 946
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Gapop 10.0 , Gapext 1.0

Searched: 2960401 seqs, 2274450654 residues

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result % Query

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2	946	100.0	946	14	US-10-066-179-1	Sequence 1, Appli
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4	840.4	88.1	1105	9	US-09-894-657-2	Sequence 2, Appli
5	833	88.1	1127	13	US-10-388-360-369	Sequence 259, App
6	799	84.5	953	10	US-09-873-367C-259	Sequence 259, App
7	799	84.5	971	17	US-10-641-643-646	Sequence 646, App
8	546	57.7	842	16	US-10-264-049-587	Sequence 587, App
9	400	42.3	477	10	US-09-918-995-27567	Sequence 27567, A
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11	344	36.4	1454	5	US-09-880-107-355	Sequence 3, Appli
12	267.2	28.2	445	9	US-10-209-967-3	Sequence 355, App
13	211.4	22.3	303	9	US-09-783-590-3437	Sequence 3437, App
14	201.2	21.3	388	9	US-09-783-590-3465	Sequence 3465, App
15	175.6	18.6	235	9	US-09-833-381-166	Sequence 166, App
16	106.2	11.2	17580	15	US-10-240-452-12	Sequence 12, Appl
17	98.6	10.4	17580	10	US-10-240-452-11	Sequence 12, Appl
18	64.4	6.8	880	10	US-09-989-993-12	Sequence 13280, A
19	60	6.3	60	10	US-09-908-975-13280	Sequence 165125,
20	59.8	6.3	848	13	US-10-027-632-165125	Sequence 165125,
21	59.8	6.3	848	16	US-10-027-632-165125	Sequence 725, App
22	49.2	5.2	108	9	US-09-728-445-725	Sequence 499, App
23	47.6	5.0	80	12	US-10-384-245-499	Sequence 2538, Ap
24	43.4	4.6	3138	15	US-10-156-761-2538	Sequence 1, Appli
25	43.4	4.6	9025608	15	US-10-156-761-1	Sequence 1, Appli
26	43.2	4.6	4266	15	US-10-156-761-5083	Sequence 28, Appl
27	43.2	4.6	9025608	15	US-10-156-761-1	Sequence 15, Appl
28	43	4.5	2984	13	US-10-399-645-28	Sequence 10, Appl
29	42.2	4.5	143899	10	US-09-972-546-15	Sequence 10, Appl
30	41.4	4.4	594	13	US-10-142-426-10	Sequence 10, Appl
31	41.4	4.4	594	15	US-10-123-155-10	Sequence 10, Appl
32	41.4	4.4	594	15	US-10-146-731-10	Sequence 10, Appl
33	41.4	4.4	594	15	US-10-140-472-10	Sequence 10, Appl
34	41.4	4.4	594	15	US-10-141-761-10	Sequence 10, Appl
35	41.4	4.4	594	15	US-10-142-885-10	Sequence 10, Appl
36	41.4	4.4	594	15	US-10-158-790-10	Sequence 10, Appl
37	41.4	4.4	594	16	US-10-137-871-10	Sequence 10, Appl
38	41.4	4.4	594	16	US-10-140-923-10	Sequence 10, Appl
39	41.4	4.4	594	16	US-10-141-756-10	Sequence 10, Appl
40	41.4	4.4	594	16	US-10-141-759-10	Sequence 10, Appl
41	41.4	4.4	594	16	US-10-140-805-10	Sequence 10, Appl
42	41.4	4.4	594	16	US-10-140-864-10	Sequence 10, Appl
43	41.2	4.4	80557	15	US-10-080-170-647	Sequence 647, App
44	40.8	4.3	1036	13	US-10-142-426-142	Sequence 142, App
45	40.8	4.3	1036	15	US-10-123-155-142	

ALIGNMENTS

RESULT 1
US-09-922-378-1
; Sequence 1, Application US/09922378
; Patent No. US20020037869A1
; GENERAL INFORMATION:

; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922,378
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-922-378-1

Query Match 100.0%; Score 946; DB 9; Length 946;
Best Local Similarity 100.0%; Pred. No. 5.5e-267;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGSCCTAGGGCGCGGCTCAGGGCCCTCAGATCGGGCTTGGGCCCGCAGAGCATGTTCAG 60
Db 1 GGSCCTAGGGCGCGGCTCAGGGCCCTCAGATCGGGCTTGGGCCCGCAGAGCATGTTCAG 60

Qy 61 ATCCAGAGTTTCAGCCGAGTGACGAGAGACTCCAGCTCTGCAGAGAGGGCCCTGGCC 120
Db 61 ATCCAGAGTTTCAGCCGAGTGACGAGAGACTCCAGCTCTGCAGAGAGGGCCCTGGCC 120

Qy 121 CCAGCCCCCGAGGGAGCGGCCCTCAGGCTCCGGCAAGCATCATCCAGAGGGCCCGCAGGC 180
Db 121 CCAGCCCCCGAGGGAGCGGCCCTCAGGCTCCGGCAAGCATCATCCAGAGGGCCCGCAGGC 180

Qy 181 CTCCTGTGGAGCCGAGTCACGAGGAGCAGCCACAGCAGCGCCATCATGTGAGGC 240
Db 181 CTCCTGTGGAGCCGAGTCACGAGGAGCAGCCACAGCAGCGCCATCATGTGAGGC 240

Qy 241 GCTGGGGCTGTGGAGATCCGAGTCGCCACAGCTCTACCCCGGGGAGCGGAGAGCGAC 300
Db 241 GCTGGGGCTGTGGAGATCCGAGTCGCCACAGCTCTACCCCGGGGAGCGGAGAGCGAC 300

Qy 301 GAAGGGATGGGGAGGAGGCCCGCCCTTTTGGGGCGGCTTCGGCGTGGGGCCCCCAGC 360
Db 301 GAAGGGATGGGGAGGAGGCCCGCCCTTTTGGGGCGGCTTCGGCGTGGGGCCCCCAGC 360

Qy 361 CTCGGGAGCAGACGCGCTATGGCCGAGCTCCGGAGGATGAGTGACGAGTTTGTGAC 420
Db 361 CTCGGGAGCAGACGCGCTATGGCCGAGCTTCGGAGGATGAGTGACGAGTTTGTGAC 420

Qy 421 TCCTTTAAGAGGGAGCTTCCTCGCCCGAAGAGCGCGGCGACAGCAAGCATGGCGCA 480
Db 421 TCCTTTAAGAGGGAGCTTCCTCGCCCGAAGAGCGCGGCGACAGCAAGCATGGCGCA 480

Qy 481 AGCTCAGCTGGAGCGAGTCTCCAGTCTGTTGGATCGGAAGCTTGGCGAGGGAGGC 540
Db 481 AGCTCAGCTGGAGCGAGTCTCCAGTCTGTTGGATCGGAAGCTTGGCGAGGGAGGC 540

Qy 541 TCCGCCCCCTCCAGTGACCTTCGTTCCATCCACATCCCGGAAATCCACCCGTTCCATTCGCCCT 600
Db 541 TCCGCCCCCTCCAGTGACCTTCGTTCCATCCACATCCCGGAAATCCACCCGTTCCATTCGCCCT 600

Db 541 TCGGCCCTCCCACTGACCTTCGGTCCACATCCCGAAATCCACCCGTTGCCCT 600
Qy 601 GGCAGCAATTTTGAATATGGGAGAGTAAGTTCCCTCAGGCTATGCAAAAAGAGAT 660
Db 601 GGCAGCAATTTTGAATATGGGAGAGTAAGTTCCCTCAGGCTATGCAAAAAGAGAT 660
Qy 661 CCGTCTGTATCTTTGGAGGAGAGTTGACCCAGATTCCTTCGGTGTGTGAAGCC 720
Db 661 CCGTCTGTATCTTTGGAGGAGAGTTGACCCAGATTCCTTCGGTGTGTGAAGCC 720
Qy 721 ACAGAAAGTTGGTCCCATCGAGATTTTGGGTTTTCGGCCACACCGCCGGAAGTGGCT 780
Db 721 ACAGAAAGTTGGTCCCATCGAGATTTTGGGTTTTCGGCCACACCGCCGGAAGTGGCT 780
Qy 781 CCGTGGCCCGCCCTCAGGTTCCGGGTTTCCCGCAGGCGCTTAAAGTAGCGAGCC 840
Db 781 CCGTGGCCCGCCCTCAGGTTCCGGGTTTCCCGCAGGCGCTTAAAGTAGCGAGCC 840
Qy 841 AGGTTAACCGTTGTGTACCCGGACCCCGGATGCGCTTAAAGTAGCGAGCC 900
Db 841 AGGTTAACCGTTGTGTACCCGGACCCCGGATGCGCTTAAAGTAGCGAGCC 900
Qy 901 GTACCAATGTTTAAAGCCCGGTGTGTGCCAAAAA 946
Db 901 GTACCAATGTTTAAAGCCCGGTGTGTGCCAAAAA 946

RESULT 2
US-10-066-179-1
; Sequence 1, Application US/10066179
; Publication No. US20020115631A1
; GENERAL INFORMATION:
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066.179
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-066-179-1

Query Match 100.0%; Score 946; DB 14; Length 946;
Best Local Similarity 100.0%; Pred. No. 5.5e-267;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCTTAGGGCCCGGGTCAAGGGCTCGAGATCGGGCTTGGGCCAGAGCATGTTCCAG 60
Db 1 GGGCTTAGGGCCCGGGTCAAGGGCTCGAGATCGGGCTTGGGCCAGAGCATGTTCCAG 60
Qy 61 ATCCACAGTTTGAAGCCGAGTACAGAGAGACTCCAGCTCTGAGAGAGGGGCTGGGC 120

Db 61 ATCCACAGTTTGAAGCCGAGTACAGAGAGACTCCAGCTCTGAGAGAGGGGCTGGGC 120
Qy 121 CCCAGCCCCGAGGGAGGGCCCTCAGGCTCCGGCAAGCATCATCGCCAGGCCCCAGGC 180
Db 121 CCCAGCCCCGAGGGAGGGCCCTCAGGCTCCGGCAAGCATCATCGCCAGGCCCCAGGC 180
Qy 181 CTCCTGTGGAGCCCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 CTCCTGTGGAGCCCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 241 GCTGGGCTGTGAGATCCGAGTCCGCAAGCTCTACCCCGGGGAGAGAGAGAGAG 300
Db 241 GCTGGGCTGTGAGATCCGAGTCCGCAAGCTCTACCCCGGGGAGAGAGAGAGAG 300
Qy 301 GAAGGAGATGGGGAG 360
Db 301 GAAGGAGATGGGGAG 360
Qy 361 CTCCTGGCAGCAG 420
Db 361 CTCCTGGCAGCAG 420
Qy 421 TCTTTTAAAG 480
Db 421 TCTTTTAAAG 480
Qy 481 AGCTCCAGCTGAG 540
Db 481 AGCTCCAGCTGAG 540
Qy 541 TCGGCCCTCCCGAGTACCTTCGGTCCACATCCCGAAATCCACCCGTTCCCATTTGCCCT 600
Db 541 TCGGCCCTCCCGAGTACCTTCGGTCCACATCCCGAAATCCACCCGTTCCCATTTGCCCT 600
Qy 601 GGGCAGCATTTTGAATATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GGGCAGCATTTTGAATATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy 661 CCGTCTGTATCTTTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 CCGTCTGTATCTTTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 721 ACAGAAAGTTGGTCCCATCGAGAGTTTGGGTTTTCGGCCACACAGCCCGGAGAGTGGCT 780
Db 721 ACAGAAAGTTGGTCCCATCGAGAGTTTGGGTTTTCGGCCACACAGCCCGGAGAGTGGCT 780
Qy 781 CCGTGGCCCGCCCTCAGGTTCCGGGTTTCCCGAGGCGCTCGCTTAAGTAGCGAGCC 840
Db 781 CCGTGGCCCGCCCTCAGGTTCCGGGTTTCCCGAGGCGCTCGCTTAAGTAGCGAGCC 840
Qy 841 AGGTTTAAACCGTTGTGTACCCGGACCCCGGATGCGCTTAAAGTAGCGAGTCA 900
Db 841 AGGTTTAAACCGTTGTGTACCCGGACCCCGGATGCGCTTAAAGTAGCGAGTCA 900
Qy 901 GTACCAATGTTTAAAGCCCGGTGTGTGCCAAAAA 946
Db 901 GTACCAATGTTTAAAGCCCGGTGTGTGCCAAAAA 946

RESULT 3

US-10-209-967-1
; Sequence 1, Application US/10209967
; Publication No. US20030171279A1
; GENERAL INFORMATION:
; APPLICANT: WUNGER, JOSHUA
; APPLICANT: ROIZMAN, BERNARD
; TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND
; FILE REFERENCE: ARCD:380US
; CURRENT APPLICATION NUMBER: US/10/209,967
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 60/308,929
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Human BAD
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(555)
US-10-209-967-1

Query Match 99.98; Score 945; DB 15; Length 945;

Best Local Similarity 100.0%; Pred.No. 1.1e-266; Mismatches 0; Indels 0; Gaps 0;
Matches 945; Conservative 0;

Qy	1	GGGCTAGGGCGCGGCTCAGGGGCTCGAGATCGGGCTTGGGCCACAGCATGTTCCAG	60
Db	1	GGGCTAGGGCGCGGCTCAGGGGCTCGAGATCGGGCTTGGGCCACAGCATGTTCCAG	60
Qy	61	ATCCAGAGTTTGAGCCGAGTGAGCAGAGAGACTCCAGCTCTGACAGAGGGGCTGGGC	120
Db	61	ATCCAGAGTTTGAGCCGAGTGAGCAGAGAGACTCCAGCTCTGACAGAGGGGCTGGGC	120
Qy	121	CCAGCCCCGAGGGGAGCGGGCCCTCAGGCTCCGGCAAGCATCATGCCAGGCCCCAGGC	180
Db	121	CCAGCCCCGAGGGGAGCGGGCCCTCAGGCTCCGGCAAGCATCATGCCAGGCCCCAGGC	180
Qy	181	CTCCTGTGGGACGCCAGTCCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	240
Db	181	CTCCTGTGGGACGCCAGTCCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	240
Qy	241	GCTGGGCTGTGGAGATCCGGAGTCCGGAGTCCGGAGTCCGGAGTCCGGAGTCCGGAG	300
Db	241	GCTGGGCTGTGGAGATCCGGAGTCCGGAGTCCGGAGTCCGGAGTCCGGAGTCCGGAG	300
Qy	301	GAGGGATGGGGGAGGAGCCGCTTTTCGGGGCCGCTTCGGGCTTCGGGCTTCGGGCTTC	360
Db	301	GAGGGATGGGGGAGGAGCCGCTTTTCGGGGCCGCTTCGGGCTTCGGGCTTCGGGCTTC	360
Qy	361	CTCTGGGAGCAGAGCCCTATGGCGGAGCTCCGGAGATGATGACAGATTGTGGAC	420
Db	361	CTCTGGGAGCAGAGCCCTATGGCGGAGCTCCGGAGATGATGACAGATTGTGGAC	420

Db	361	CTCTGGGAGCAGAGCCCTATGGCGGAGCTCCGGAGATGATGAGAGATTGTGGAC	420
Qy	421	TCCTTTAAGAGAGGACTTCTCGCCCGAAGAGCGCGGCGCACAGCAACGACAGATGGGCAA	480
Db	421	TCCTTTAAGAGAGGACTTCTCGCCCGAAGAGCGCGGCGCACAGCAACGACAGATGGGCAA	480
Qy	481	AGCTCCAGCTGGAGCGGAGTCTCCAGTCTGCTGGTGGATCGGAATTGGGACGGGAGGC	540
Db	481	AGCTCCAGCTGGAGCGGAGTCTCCAGTCTGCTGGTGGATCGGAATTGGGACGGGAGGC	540
Qy	541	TCGGCCCCCTCCCAAGTGCCTTCGGTCCACATCCCGAAATCCACCCGTTCCCATTCGCCCT	600
Db	541	TCGGCCCCCTCCCAAGTGCCTTCGGTCCACATCCCGAAATCCACCCGTTCCCATTCGCCCT	600
Qy	601	GGGAGCCATTTTGAATATGGGAGAGTAAGTTCCTCAGGCTTATGCAAAAAGAGAT	660
Db	601	GGGAGCCATTTTGAATATGGGAGAGTAAGTTCCTCAGGCTTATGCAAAAAGAGAT	660
Qy	661	CGTGTGTATTCCTTTGGAGGGAGGGTTGACCCAGATTCCCTTCCGGTGTGTGAAGCC	720
Db	661	CGTGTGTATTCCTTTGGAGGGAGGGTTGACCCAGATTCCCTTCCGGTGTGTGAAGCC	720
Qy	721	ACGGAAGTTGGTCCCATCGGAAGTTTGGGTTTTCGCCACACAGCCCGGAGTGGCT	780
Db	721	ACGGAAGTTGGTCCCATCGGAAGTTTGGGTTTTCGCCACACAGCCCGGAGTGGCT	780
Qy	781	CGTGGCCCCGCTCAGCTTCGGGTTTCCCGAGGCGCTGCGCTTAAGTAGCGAGCC	840
Db	781	CGTGGCCCCGCTCAGCTTCGGGTTTCCCGAGGCGCTGCGCTTAAGTAGCGAGCC	840
Qy	841	AGGTTTAAACGTTGTGTACCGGGACCCGAGCCCCCGCATGCTTGGGGCCCGTGATCA	900
Db	841	AGGTTTAAACGTTGTGTACCGGGACCCGAGCCCCCGCATGCTTGGGGCCCGTGATCA	900
Qy	901	GTACCAATGTATTAAGCCCGGCTGTGTGCCAAAAA	945
Db	901	GTACCAATGTATTAAGCCCGGCTGTGTGCCAAAAA	945

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Job time : 512 secs

OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 13:36:04 ; Search time 2957 Seconds
(without alignments)
9553.474 Million cell updates/sec

Title: US-09-922-378-1
Perfect score: 946
Sequence: 1 gggcgctggcgccgggtca.....gtgtgcaaaaaaaaaaaaaa 946

Scoring table: IDENTITY NUC
Capop 10.0 , Capext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estrov:*
 - 6: em_estrpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_man:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rtd:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrt:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	778.2	82.3	1001	13	BQ276268
2	776.6	82.1	920	12	BG748558
3	766.4	81.0	867	12	BI917840
4	764.8	80.8	873	12	BG742674
5	758.8	80.2	949	12	BG752050
6	751	79.4	880	12	BI756192
7	749.8	79.3	1005	12	BM919507
8	736	77.8	907	13	BQ933058
9	722.2	76.3	933	12	BI669797
10	719.4	76.0	1024	12	BM811187
11	703	74.3	908	14	CA488765
12	702.4	74.2	767	14	CA426410
13	697.4	73.7	773	12	BI870839
14	696.4	73.6	764	14	CF541292
15	692.8	73.2	887	14	CA488397
16	692	73.2	1050	12	BM557474
17	690.4	73.0	889	12	BI757416
18	688.8	72.8	811	14	CF455210
19	685.6	72.5	761	12	BM973320
20	678.6	71.7	870	14	CD245697
21	678	71.7	920	13	BQ963001
22	674.8	71.3	1170	12	BM464317
23	674.2	71.3	888	13	BQ216214
24	673.8	71.2	891	9	AI338346
25	672.8	71.1	756	12	BI818504
26	669.6	70.8	727	14	CF126337
27	667.4	70.5	807	13	EX415776
28	665.6	70.4	880	13	BQ989089
29	663	70.1	873	12	BQ289203
30	661.4	69.9	791	12	BG818638
31	658.2	69.6	885	13	BQ420314
32	656.4	69.4	907	12	BG522766
33	655.2	69.3	804	12	BI836511
34	648.6	68.6	703	13	EX093156
35	647	68.4	777	12	BG749431
36	647	68.4	912	13	BUI82782
37	641.8	67.8	1125	12	BM805363
38	638.2	67.5	706	12	BG748336
39	635.4	67.2	691	12	BG707618
40	631.2	66.7	727	12	BGI49833
41	619	65.4	1100	12	BG282723
42	618.2	65.3	1060	12	BM424198
43	613.2	64.8	923	14	CA495333
44	605	64.0	772	12	BG748347
45	603	63.7	722	9	AI813350

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Job time : 2965 secs